

178579

**From:** Sullivan, Daniel  
**Sent:** Friday, February 03, 2006 2:42 PM  
**To:** STIC-Biotech/ChemLib  
**Subject:** Sequence search request 09846456

Please search for the following in the issued patent and commercial databases:

An oligo search of SEQ ID NO: 1, 2, 3 and 5.

Thank you.

**Daniel M. Sullivan**

Examiner AU 1636

Remsen Bldg.

Room 2A74

Tel: (571) 272-0779

Mailbox: 2C70

FEB - 3 2006  
SEARCHED (STIC)  
INDEXED (STIC)  
SERIALIZED (STIC)

Oligo search was not done, per our phone conversation. To do the regular plus oligo searches would add up to about 28 hrs, and our limit w/o special permission is 20 hours.

If these results are not adequate, we can figure out how to proceed. Let me know if you require further work.

Monica Reck  
Ext. 22524

\*\*\*\*\*  
 Searcher: \_\_\_\_\_  
 Searcher Phone: \_\_\_\_\_  
 Date Searcher Picked up: \_\_\_\_\_  
 Date completed: \_\_\_\_\_  
 Searcher Prep Time: \_\_\_\_\_  
 Online Time: \_\_\_\_\_

\*\*\*\*\*  
 Type of Search  
 NA# \_\_\_\_\_ AA# \_\_\_\_\_  
 S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
 Encode/Transl: \_\_\_\_\_  
 Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
 Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*  
 Vendors and cost where applicable  
 STN: \_\_\_\_\_  
 DIALOG: \_\_\_\_\_  
 QUESTEL/ORBIT: \_\_\_\_\_  
 LEXIS/NEXIS: \_\_\_\_\_  
 SEQUENCE SYSTEM: \_\_\_\_\_  
 WWW/Internet: \_\_\_\_\_  
 Other (Specify): \_\_\_\_\_

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using bw model

Run on: February 8, 2006, 23:04:12 ; Search time 546.227 Seconds  
(6546.426 Million cell updates/sec)

Title: US-09-846-456A-5

Perfect score: 159

Sequence: 1 ttaatgaccaggccacggcg.....ctttcagaaagaacaaaca 159

Scoring table: IDENTITY\_NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing First 45 summaries

Database : GenBml:  
1: gb\_ba:  
2: gb\_in:  
3: gb\_env:  
4: gb\_om:  
5: gb\_ov:  
6: gb\_pat:  
7: gb\_ph:  
8: gb\_pr:  
9: gb\_ro:  
10: gb\_sts:  
11: gb\_sy:  
12: gb\_un:  
13: gb\_vl:  
14: gb\_htgi:  
15: gb\_pl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	159	100.0	159	6	AX351033		AX351033 Sequence
2	159	100.0	357	6	AX351030		AX351030 Sequence
3	155.8	98.0	10442	6	CS031389		CS031389 Sequence
4	155.8	98.0	10442	6	CS043341		CS043341 Sequence
5	155.8	98.0	10442	6	CS108251		CS108251 Sequence
6	155.8	98.0	10442	6	AR607250		AR607250 Sequence
7	155.8	98.0	10442	6	AR628825		AR628825 Sequence
8	155.8	98.0	10442	6	AX060713		AX060713 Sequence
9	155.8	98.0	10442	6	AX060892		AX060892 Sequence
10	155.8	98.0	10442	8	AF285167		AF285167 Homo sapi
11	155.8	98.0	10474	6	AR607255		AR607255 Sequence
12	155.8	98.0	10474	6	AR607256		AR607256 Sequence
13	155.8	98.0	10474	6	AR628830		AR628830 Sequence
14	155.8	98.0	10474	6	AR628831		AR628831 Sequence
15	155.8	98.0	10474	6	AX060719		AX060719 Sequence
16	155.8	98.0	10474	6	AX060721		AX060721 Sequence
17	155.8	98.0	10474	6	AX060898		AX060898 Sequence
18	155.8	98.0	10474	6	AX060900		AX060900 Sequence

19 155.8 98.0 149034 8 AF275948 Homo sapi  
20 153.2 96.4 183999 6 AX025899 Sequence  
21 143.4 90.2 697 8 AF256627 Homo sapi  
22 142.2 89.4 200 8 AF256233S2  
23 142.2 89.4 446 6 AX127764 Sequence  
24 142.2 89.4 446 6 AX137751 Sequence  
25 142.2 89.4 447 6 BD117945 EST and e  
26 142.2 89.4 447 6 AR423392 Sequence  
27 142.2 89.4 447 6 AX983086 Sequence  
28 142.2 89.4 480 8 HSA252277 Homo sapi  
29 142.2 89.4 1062 6 AR583753 Sequence  
30 142.2 89.4 1062 6 AX616417 Sequence  
31 142.2 89.4 7260 6 AX253452 Sequence  
32 142.2 89.4 9741 6 AX127830 Sequence  
33 142.2 89.4 9741 6 AX139817 Sequence  
34 142.2 89.4 9741 6 AX351038 Sequence  
35 142.2 89.4 9854 6 AX127831 Sequence  
36 142.2 89.4 9854 6 AX139818 Sequence  
37 142.2 89.4 10412 6 CQ785966 Sequence  
38 142.2 89.4 10412 6 CQ981355 Sequence  
39 142.2 89.4 10412 6 CS031387 Sequence  
40 142.2 89.4 10412 6 CS036636 Sequence  
41 142.2 89.4 10412 6 CS040339 Sequence  
42 142.2 89.4 10412 6 CS045588 Sequence  
43 142.2 89.4 10545 6 AR393442 Sequence  
C 44 142.2 89.4 12608 8 AL353685 Human DNA  
C 45 142.2 89.4 175064 14 AC012230 Homo sapi  
AC012230 Homo sapi

## ALIGNMENTS

RESULT 1  
AX351033 LOCUS AX351033 Sequence 5 from Patent WO18374746.  
DEFINITION Sequence AX351033  
ACCESSION AX351033  
VERSION AX351033.1 GI:18616389  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE  
AUTHORS Rosier-Montus M.F., Prades C., Lemoine C., Naudin L., Denetle P.,  
Brewer B., Duverger N., Remaley A., and Santamarina-Fojo S.  
TITLE Regulatory nucleic acid sequences of the abci gene  
JOURNAL Patent: WO 0183746-A 5 08-NOV-2001;  
Aventis Pharma S.A. (FR)  
FEATURES Location,Qualifiers  
1. .159  
SOURCE /organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 159; DB 6; Length 159;  
Best Local Similarity 100.0%; Pred. No. 3 2e-32;  
Matches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATGACCAGCCACGGGCCTCCCTGTCAAGCTGGCCCTTCAGGACTCTCCC 60  
Db 1 TTATGACCAGCCACGGGCCTCCCTGTCAAGCTGGCCCTTCAGGACTCTCCC 60

Qy 61 GAGGCCACAGCTGGCGCTGGCGCTAGGGACATGGCATTTGGCTCAGCTGAGTGT 120  
Db 61 GAGGCCACAGCTGGCGCTGGCGCTAGGGACATGGCATTTGGCTCAGCTGAGTGT 120

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	159	100.0	159	6	AX351033		AX351033 Sequence
2	159	100.0	357	6	AX351030		AX351030 Sequence
3	155.8	98.0	10442	6	CS031389		CS031389 Sequence
4	155.8	98.0	10442	6	CS043341		CS043341 Sequence
5	155.8	98.0	10442	6	CS108251		CS108251 Sequence
6	155.8	98.0	10442	6	AR607250		AR607250 Sequence
7	155.8	98.0	10442	6	AR628825		AR628825 Sequence
8	155.8	98.0	10442	6	AX060713		AX060713 Sequence
9	155.8	98.0	10442	6	AX060892		AX060892 Sequence
10	155.8	98.0	10442	8	AF285167		AF285167 Homo sapi
11	155.8	98.0	10474	6	AR607255		AR607255 Sequence
12	155.8	98.0	10474	6	AR607256		AR607256 Sequence
13	155.8	98.0	10474	6	AR628830		AR628830 Sequence
14	155.8	98.0	10474	6	AR628831		AR628831 Sequence
15	155.8	98.0	10474	6	AX060719		AX060719 Sequence
16	155.8	98.0	10474	6	AX060721		AX060721 Sequence
17	155.8	98.0	10474	6	AX060898		AX060898 Sequence
18	155.8	98.0	10474	6	AX060900		AX060900 Sequence

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	159	100.0	159	6	AX351033		AX351033 Sequence
2	159	100.0	357	6	AX351030		AX351030 Sequence
3	155.8	98.0	10442	6	CS031389		CS031389 Sequence
4	155.8	98.0	10442	6	CS043341		CS043341 Sequence
5	155.8	98.0	10442	6	CS108251		CS108251 Sequence
6	155.8	98.0	10442	6	AR607250		AR607250 Sequence
7	155.8	98.0	10442	6	AR628825		AR628825 Sequence
8	155.8	98.0	10442	6	AX060713		AX060713 Sequence
9	155.8	98.0	10442	6	AX060892		AX060892 Sequence
10	155.8	98.0	10442	8	AF285167		AF285167 Homo sapi
11	155.8	98.0	10474	6	AR607255		AR607255 Sequence
12	155.8	98.0	10474	6	AR607256		AR607256 Sequence
13	155.8	98.0	10474	6	AR628830		AR628830 Sequence
14	155.8	98.0	10474	6	AR628831		AR628831 Sequence
15	155.8	98.0	10474	6	AX060719		AX060719 Sequence
16	155.8	98.0	10474	6	AX060721		AX060721 Sequence
17	155.8	98.0	10474	6	AX060898		AX060898 Sequence
18	155.8	98.0	10474	6	AX060900		AX060900 Sequence

result	No.	Score	Query	Match	Length	DB	ID	Description
1	159	100.0	159	6	AAD37269	Human ABC		Aad37269 Human ABC
2	159	100.0		357	6	ADD37266		Aad37266 Human ABC
3	159	100.0		357	6	ABL58148		Abi58148 Human ABC
4	157.4	99.0		159	6	ABN99235		Abn99235 Polymorph
5	155.8	98.0		10365	10	ADD94068		Add94068 Human ATP
6	155.8	98.0		10381	10	ADD94069		Add94069 Human ATP
7	155.8	98.0		10423	10	ADD94070		Add94070 Human ATP
8	155.8	98.0		10442	4	AAF24680		Aaf24680 Nucleotid
9	155.8	98.0		10442	4	AAF24702		Aaf24702 Nucleotid
10	155.8	98.0		10442	13	ADP23549		Adp23549 PRO polyp
11	155.8	98.0		10442	14	ADY15089		Ady15089 DNA encod
12	155.8	98.0		10442	14	ARA23717		Ara23717 Human PRO
13	155.8	98.0		10474	4	AAF24655		Aaf24685 Nucleotid
14	155.8	98.0		10474	4	AAF24666		Aaf24686 Nucleotid
15	155.8	98.0		10474	4	AAF24708		Aaf24708 Nucleotid
16	155.8	98.0		10474	4	AAF24707		Aaf24707 Nucleotid
17	155.8	98.0		149034	11	ADP65433		Adp65433 Human ABC
18	153.2	96.4		183999	13	ADP92811		Aad92811 Human ABC
19	153.2	96.4		183999	13	ABN9234		Abn9234 Polymorph
20	147	92.5		158	6	ABN9234		Add41442 Myocardia
21	143.4	90.2		201	13	ADD41442		Add41442 Myocardia
22	143.4	90.2		201	13	ADD44225		Add44225 Myocardia
23	143.4	90.2		201	13	ADQ14200		Adq14200 Myocardia
24	143.4	90.2		1402	13	ADQ14200		Adq14200 Myocardia
25	143.4	90.2		1859	13	ADQ8534		Adq8534 Human SNA
26	143.4	90.2		10405	13	ADQ8535		Adq8535 Human SNA
27	142.2	89.4		446	4	AAS04035		Aas04035 Partial h
28	142.2	89.4		1062	8	ACC5110		Acc5110 Human hAB
29	142.2	89.4		7086	4	ABA0200		Aba0200 Human ABC
30	142.2	89.4		7086	4	AAK5667		Aak5667 Human pol
31	142.2	89.4		7260	4	AAT0315		Aat0315 Human ATP
32	142.2	89.4		7260	4	ADD2326		Add2326 Human ATP
33	142.2	89.4		7281	4	AAK51683		Aak51683 Human pol
34	142.2	89.4		9741	4	AAS05120		Aas05120 Human ABC
35	142.2	89.4		9741	6	ADD37273		Add37273 Human ABC
36	142.2	89.4		9741	6	ABLS5146		Abi5146 Human ABC
37	142.2	89.4		9854	4	AAS06121		Aas06121 Human ABC
38	142.2	89.4		9870	6	ABN99307		Abn99307 Polymorph
39	142.2	89.4		9870	6	ABN99302		Abn99302 Polymorph
40	142.2	89.4		9870	6	ABN99305		Abn99305 Polymorph
41	142.2	89.4		9870	6	ABN99317		Abn99317 Polymorph
42	142.2	89.4		9870	6	ABN99321		Abn99321 Polymorph
43	142.2	89.4		9870	6	ABN99323		Abn99323 Polymorph
44	142.2	89.4		9870	6	ABN99309		Abn99309 Polymorph
45	142.2	89.4		9870	6	ABN99329		Abn99329 Polymorph

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2006, 15:01:42 ; Search time 444.338 Seconds  
(without alignments)  
16742.090 Million cell updates/sec

Title: US-09-846-456A-5

Perfect score: 159

Sequence: 1 ttatgaccaggcacggcg.....cttcagaagaagacaaaca 159

Scoring table: IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 0%  
Listing first 45 summaries

Database : EST:  
 1: qb\_est1:  
 2: qb\_est2:  
 3: qb\_est3:  
 4: qb\_htc:  
 5: qb\_est4:  
 6: qb\_est5:  
 7: qb\_est6:  
 8: qb\_est7:  
 9: qb\_gss1:  
 10: qb\_gss2:  
 11: qb\_gss3:  
\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	155.8	98.0	547	1 AL698654	AL698654 DKFZp686N12109
2	155.8	98.0	583	2 BP280727	BP280727 BP280727
3	155.8	98.0	595	3 BP280045	BP280045 BP280045
4	142.2	89.4	583	4 BP200657	BP200657 BP200657
5	142.2	89.4	583	5 BP287529	BP287529 BP287529
6	142.2	89.4	663	5 BX955241	BX955241 DKFZp686N12109
7	140.6	88.4	663	6 AU135588	AU135588 AU135588
8	105.4	66.3	648	7 BB657864	BB657864 BB657864
9	72.8	45.8	619	8 BB657864	BB657864 BB657864
10	72.8	45.8	4783	9 AK051920	AK051920 Mus muscu
11	70.8	44.5	292	10 BX901916	BX901916 BX901916
12	70.8	44.5	535	11 CG384217	CG384217 CG384217
13	54	34.0	490	12 DN853427	DN853427 DN853427
14	44.8	28.2	668	13 CX260141	CX260141 CX260141
15	44.8	28.2	742	14 BX911478	BX911478 BX911478
16	44	27.7	862	15 CO927141	CO927141 CO927141
17	43.4	27.3	641	16 BJ901916	BJ901916 BJ901916
18	42.6	26.8	1284	17 CNS0EXPH	CNS0EXPH CNS0EXPH
19	40	25.2	340	18 BY175500	BY175500 BY175500
20	39.8	25.0	696	19 CO352299	CO352299 CO352299
c 21	38.4	24.2	605	20 AJ732100	AJ732100 AJ732100
22	38.4	24.2	687	21 AJ732095	AJ732095 AJ732095

## ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	DEPOSITION	VERSION	KEYWORDS	SOURCE	ORGANISM	COMMENT
AL698654	DKFZp686N12109	547 bp mRNA (synonym: hlcc3) Homo sapiens cDNA clone	DKFZp686N12109	5	GI:19619194			MIPS
			DKFZp686N12109	5				Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
			DKFZp686N12109	5				This is the 5' sequence of the clone insert
								Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; consortium of the German Genome Project.
								No sl sequence available.
								This clone (DKFZp686N12109) is available at the RZPD in Berlin.
								Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
								Contact: Mips
								1. -547
								EST (Muererhoeft, et al.)
								Unpublished (1999)
								REFERENCE
								AUTHORS
								Duesterhoeft, A., Lauber, J., Newes, H.W., Gassenhuber, J. and Wiemann, S.
								TITLE
								JOURNAL
								EST (Muererhoeft, et al.)
								COMMENT
								MIPS

ORIGIN

Query Match 98.0%; Score 155.8; DB 1; Pred. No. 3.1e-33;

Best local Similarity 98.7%; Length 547;

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using bw model

Run on: February 10, 2006, 19:02:01 ; Search time 90.4911 Seconds  
(without alignments)  
14529.947 Million cell updates/sec

Title: US-09-846-456a-5

Perfect score: 159

Sequence: 1 ttaatgaccaggccacgggg.....ctttcagaaaaacaaaca 159

Scoring table: IDENTITY\_NUC Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing First 45 summaries

RESULT 1  
US-09-846-456-5

; Sequence 5, Application US/09846456  
; Patent No. US20020146792A1  
; GENERAL INFORMATION:  
; APPLICANT: Robier, Marie  
; APPLICANT: Prades, Catherine  
; APPLICANT: Lemoine, Cendrine  
; APPLICANT: Naudin, Laurent  
; APPLICANT: Denefle, Patrice  
; APPLICANT: Duverger, Nicolas  
; APPLICANT: Brewar, Alan  
; APPLICANT: Remaley, Alan  
; APPLICANT: Pijo, Silvia  
; TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying  
; CURRENT APPLICATION NUMBER: US/09/B46,456  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/201,280  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 159  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-09-846-456-5

Qy 1 TTATGACCAGGCCACGGGTCCCTGCTGCAAGCTTCAGCTGAGCTCCC 60  
Query Match 100.0%; Score 159; DB 3; Length 159;  
Best Local Similarity 100.0%; Pred. No. 3 8e-43;  
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Database : Published Applications NA\_Main:\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:  
2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:  
3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:  
4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:  
5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:  
6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:  
7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:  
8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:  
9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:  
\*  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	159	100.0	159	3	US-09-846-456-5
2	159	100.0	357	3	US-09-846-456-2
3	159	100.0	357	3	US-09-846-827-4
4	157.4	99.0	159	3	US-09-984-827-26
5	155.8	98.0	10365	5	US-10-098-939-1
6	155.8	98.0	10381	5	US-10-098-939-2
7	155.8	98.0	10423	9	US-10-098-939-3
8	155.8	98.0	10442	8	US-10-920-989-1
9	155.8	98.0	10442	9	US-10-922-936-1
10	155.8	98.0	10474	8	US-10-920-989-7
11	155.8	98.0	10474	8	US-10-920-989-9
12	155.8	98.0	10474	9	US-10-922-936-7
13	155.8	98.0	10474	9	US-10-922-936-7
14	155.8	98.0	149034	9	US-10-972-836-9
15	153.2	96.4	183999	7	US-10-705-377-1
16	153.2	96.4	183999	8	US-10-874-827-25
17	147	92.5	158	3	US-09-846-827-25
18	143.4	90.2	201	8	US-10-719-993-1710
19	143.4	90.2	201	8	US-10-719-993-1768
20	143.4	90.2	201	8	US-10-719-993-1793
21	143.4	90.2	201	8	US-10-719-993-10219
22	143.4	90.2	201	8	US-10-741-600-5805
23	143.4	90.2	201	8	US-10-741-600-5863

ALIGNMENTS

Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 22:47:42 ; Search time 42:2643 Seconds  
(without alignments)  
3382.690 Million cell updates/sec

Title: US-09-846-456A-5

Perfect Score: 159

Sequence: 1 ttatgaccaggccacggcgcccccttcagaagaagacaaaca 159

Scoring table: IDENTITY\_NUC Gapop 10-0 , Gapext 1.0

Searched: 6240305 seqs, 449581930 residues

Total number of hits satisfying chosen parameters: 12480610

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_NA\_New.\*

1: /cgn2\_6/ptodata/1/pubnra/US08\_NEW\_PUB.seq;\*  
2: /cgn2\_6/ptodata/1/pubnra/US06\_NEW\_PUB.seq;\*  
3: /cgn2\_6/ptodata/1/pubnra/US07\_NEW\_PUB.seq;\*  
4: /cgn2\_6/ptodata/1/pubnra/US01\_NEW\_PUB.seq;\*  
5: /cgn2\_6/ptodata/1/pubnra/US09\_NEW\_PUB.seq;\*  
6: /cgn2\_6/ptodata/1/pubnra/US10\_NEW\_PUB.seq;\*  
7: /cgn2\_6/ptodata/1/pubnra/US10\_NEW\_PUB.seq;\*  
8: /cgn2\_6/ptodata/1/pubnra/US11\_NEW\_PUB.seq;\*  
9: /cgn2\_6/ptodata/1/pubnra/US11\_NEW\_PUB.seq;\*  
10: /cgn2\_6/ptodata/1/pubnra/US11\_NEW\_PUB.seq;\*  
11: /cgn2\_6/ptodata/1/pubnra/US11\_NEW\_PUB.seq;\*  
12: /cgn2\_6/ptodata/1/pubnra/US60\_NEW\_PUB.seq;\*

Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	143.4	90.2	201	7	US-10-995-561-3388	Sequence 3388, App
2	143.4	90.2	201	7	US-10-995-561-3411	Sequence 3411, App
3	143.4	90.2	201	7	US-10-995-561-3429	Sequence 3429, App
4	143.4	90.2	201	7	US-10-995-561-23954	Sequence 23954, App
5	143.4	90.2	1402	7	US-10-995-561-85	Sequence 85, App
6	143.4	90.2	1859	7	US-10-995-561-84	Sequence 84, App
7	143.4	90.2	10405	7	US-10-995-561-83	Sequence 83, App
8	143.4	90.2	159138	7	US-10-995-561-13230	Sequence 13230, App
9	142.2	89.4	10412	11	US-11-055-3094-7	Sequence 7, App
10	64.4	40.5	6786	11	US-11-055-3094-8	Sequence 8, App
11	57	35.8	201	7	US-10-995-561-24507	Sequence 24507, App
12	34.6	21.8	6768	11	US-11-043-889-1	Sequence 1, App
13	34.6	21.8	168516	11	US-11-121-086-3	Sequence 3, App
14	33.2	20.9	6432	11	US-11-043-889-3	Sequence 3, App
15	31.2	19.6	5571	7	US-10-750-185-33588	Sequence 53588, App
16	31.2	19.6	15057	11	US-11-124-367A-5010	Sequence 5010, App
17	31.2	19.6	15571	7	US-10-750-623-33588	Sequence 5015, App
18	31.2	19.6	16139	11	US-11-124-367A-5015	Sequence 42, App
C 19	30.4	19.1	155515	11	US-11-112-908-43	Sequence 43, App
C 20	30.4	19.1	159660	11	US-11-112-908-43	Sequence 41, App
C 21	30.4	19.1	177623	11	US-11-112-908-41	TED WITH

## ALIGNMENTS

RESULT 1  
US-10-995-561-3388  
; Publication No. US/10995561  
; Publication No. US2005027204A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF DETECTION AND USES THEREOF  
; TITLE OF INVENTION: FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 20/04-11-24  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: PasteSEQ for Windows Version 4.0  
; SEQ ID NO: 3388  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-995-561-3388

Query Match	Best Local Similarity	Score 143.4;	DB 7;	Length 201;
Matches 155;	Conservative	90.2%;	Pred. No. 3.5e-33;	Indels 1;
	Mismatches 1;	97.5%;	Gaps 1;	

Qy 1 TTAATGACCACTGGCGCTGCCTGTCAGCTCTGGCCCTGCCCTCCGGCTCC 60  
Db 27 TTATGACCACTGGCGCTGCCTGTCAGCTCTGGCCCTGCCCTCCGGCTCC 85

Qy 61 GACCCACAGCTGGGGCTGMCCTGGGGACATGGCATGTTGGCTTCACTGGCTTG 120  
Db 86 GACCCACAGCTGGGGCTGMCCTGGGGACATGGCATGTTGGCTTCACTGGCTTG 145

Qy 121 CTCCT  
Db 146 CTCCT

A 159  
A 184

Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 8, 2006, 23:04:12 ; Search time 9938.59 seconds  
 (without alignments)  
 16546.426 Million cell updates/sec

Title: US-09-846-456A-3

Perfect score: 2893

Sequence: 1 acaggccatggcagggtg.....ctagtcccgaaaaacccc 2893

Scoring table: IDENTITY\_NUC  
 Gapov 10\_0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing First 45 summaries

Database : GenBml:  
 1: qb\_ba:  
 2: qb\_in:  
 3: qb\_env:  
 4: qb\_om:  
 5: qb\_ov:  
 6: qb\_pat:  
 7: qb\_ph:  
 8: qb\_pr:  
 9: qb\_ro:  
 10: qb\_sts:  
 11: qb\_sy:  
 12: qb\_un:  
 13: qb\_vl:  
 14: qb\_htg:  
 15: qb\_pl:  
 16: qb\_dpl:  
 17: qb\_dhtg:  
 18: qb\_dpl:  
 19: qb\_dhtg:  
 20: qb\_dpl:  
 21: qb\_dhtg:  
 22: qb\_dpl:  
 23: qb\_dhtg:  
 24: qb\_dpl:  
 25: qb\_dhtg:  
 26: qb\_dpl:  
 27: qb\_dhtg:  
 28: qb\_dpl:  
 29: qb\_dhtg:  
 30: qb\_dpl:  
 31: qb\_dhtg:  
 32: qb\_dpl:  
 33: qb\_dhtg:  
 34: qb\_dpl:  
 35: qb\_dhtg:  
 36: qb\_dpl:  
 37: qb\_dhtg:  
 38: qb\_dpl:  
 39: qb\_dhtg:  
 40: qb\_dpl:  
 41: qb\_dhtg:  
 42: qb\_dpl:  
 43: qb\_dhtg:  
 44: qb\_dpl:  
 45: qb\_dhtg:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	2893	100.0	2893	6	AX351031	AX351031 Sequence
2	2893	100.0	3231	6	AX351029	AX351029 Sequence
3	2790.2	96.4	183999	6	AK092589	AK092589 Sequence
c 4	2683.6	96.2	9617	8	AL359182	AL359182 Human DNA
5	2681.8	90.5	201144	8	AF287262	AF287262 Homo sapi
c 6	1973.6	68.2	183930	14	AC160520	AC160520 Papio ham
c 7	1878	64.9	200920	14	AC161030	AC161030 Colobus g
8	1435	49.6	149034	8	AF275948	AF275948 Homo sapi
9	1394.4	48.2	1643	6	AR07251	AR07251 Sequence
10	1394.4	48.2	1643	6	AR628826	AR628826 Sequence
11	1394.4	48.2	1643	6	AX060715	AX060715 Sequence
12	1394.4	48.2	1643	6	AX060894	AX060894 Sequence
c 13	1393.8	48.2	183118	14	AC160722	AC160722 Aotus nan
c 14	1324.4	46.1	206547	14	AC161097	AC161097 Callithcebu
c 15	1317.6	45.5	198224	14	AC161090	AC161090 Callithri
16	1077.8	35.5	1197	6	AR575615	AR575615 Sequence
17	1010.4	34.9	248237	14	AC160525	AC160525 Saimiri b
18	869.8	30.8	175064	14	AC012230	AC012230 Homo sapi

## ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	SOURCE	ORGANISM	KEYWORDS	REFERENCE
1	AX351031	Sequence 3 from Patent	W00183746.					
			AX351031	GI:18616387				
					Homo sapiens (human)	Homo sapiens		
					Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.			
					Rosier-Montus,M.F., Prades,C., Lemoine,C., Naudin,L., Denfle,P., Brewer,B., Duverger,N., Remaury,A. and Santamarina-Pojo,S.			AUTHORS
					Regulatory nucleic acid sequences of the abcl gene			TITLE
					Patent: WO 0183746-A 3 0-NOV-2001;			JOURNAL
					Aventis Pharma S.A. (FR)			FEATURES
					Location/Qualifiers			Source
					1..2893	/organism="Homo sapiens"		
						/mol type="unassigned DNA"		
						/db_xref="taxon:9606"		

Query Match 100.0%; Score 2893; DB 6; Length 2893;  
 Best Local Similarity 100.0%; Pairs. No. 0;  
 Matches 2893; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAGGGCATGTTGGCAGGGTCTGTAATCTGAGTTACTCGGAGTGGGTGATGA 60  
 Db 1 ACAGGGCATGTTGGCAGGGTCTGTAATCTGAGTTACTCGGAGTGGGTGATGA 60  
 61 GCCCACATGCCACATTGCACTCCAGGCTGGCAACAAGGTAAACTCCATCTCAATT 120  
 61 GCCCACATGCCACATTGCACTCCAGGCTGGCAACAAGGTAAACTCCATCTCAATT 120  
 61 GCCCACATGCCACATTGCACTCCAGGCTGGCAACAAGGTAAACTCCATCTCAATT 120

Qy 121 AAAA.....AGAATGATATTGGTGTGACTTCATAAGTAGGAGAACGGAGAGG 180  
 Db 121 AAAA.....AGAATGATATTGGTGTGACTTCATAAGTAGGAGAACGGAGAGG 180  
 121 AAAA.....AGAATGATATTGGTGTGACTTCATAAGTAGGAGAACGGAGAGG 180

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Biocceleration Ltd.

## OM nucleic - nucleic search, using sw model

Run on: February 8, 2006, 17:12:15 ; Search time 1200.33 Seconds  
(without alignments)  
16062.998 Million cell updates/sec

Title: US-09-846-456A-3

Perfect score: 2893  
Sequence: 1 acaggccatggcggaggtg.....ctagtccggaaaaacc 2893

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993394

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing First 45 summaries

Database :

- 1: Geneseqn21;\*
- 2: Geneseqn1900b;\*
- 3: Geneseqn1900b;\*
- 4: Geneseqn2000b;\*
- 5: Geneseqn2001bs;\*
- 6: Geneseqn2002as;\*
- 7: Geneseqn2002bs;\*
- 8: Geneseqn2003ab;\*
- 9: Geneseqn2003bs;\*
- 10: Geneseqn2003cs;\*
- 11: Geneseqn2003db;\*
- 12: Geneseqn2004ab;\*
- 13: Geneseqn2004bs;\*
- 14: Geneseqn2005b;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2893	100.0	2893	6 ABN92232	Abn92232 Human ABC
2	2893	100.0	2910	6 AAD37267	Aad37267 Human ABC
3	2893	100.0	3231	6 AA037265	Aad37265 Human ABC
4	2893	100.0	3231	6 ABU58147	Abu58147 Human ABC
5	2891.4	99.9	2893	6 ABN9356	Abn9356 Polymorph
6	2891.4	99.9	2893	6 ABN9342	Abn9342 Polymorph
7	2891.4	99.9	2893	6 ABN9354	Abn9354 Polymorph
8	2891.4	99.9	2893	6 ABN9340	Abn9340 Polymorph
9	2891.4	99.9	2893	6 ABN9345	Abn9345 Polymorph
10	2891.4	99.9	2893	6 ABN9347	Abn9347 Polymorph
11	2891.4	99.9	2893	6 ABN9336	Abn9336 Polymorph
12	2891.4	99.9	2893	6 ABN9339	Abn9339 Polymorph
13	2891.4	99.9	2893	6 ABN9352	Abn9352 Polymorph
14	2891.4	99.9	2893	6 ABN9341	Abn9341 Polymorph
15	2891.4	99.9	2893	6 ABN9348	Abn9348 Polymorph
16	2891.4	99.9	2893	6 ABN9357	Abn9357 Polymorph
17	2891.4	99.9	2893	6 ABN9344	Abn9344 Polymorph
18	2891.4	99.9	2893	6 ABN9351	Abn9351 Polymorph
19	2891.4	99.9	2893	6 ABN9353	Abn9353 Polymorph

Human ABC1 transporter gene promoter.

XX Human; ABC1; transporter; ATP-binding cassette;

XX high density lipoprotein; HDL; cholesterol; familial HDL deficiency;

XX Tangier disease; myocardial infarction; atherosclerosis;

XX cardiovascular disease; Promoter; ds.

XX Homo sapiens.

XX OS

XX PN WO200236770-A2.

XX PD 10-MAY-2002.

XX XX 12-OCT-2001; 2001WO-FR003182.

XX PR 31-OCT-2000; 2000FR-0014037.

XX PR 11-DEC-2000; 2000US-0254108P.

XX PA (AVET ) AVENTIS PHARMA SA.

XX PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.

XX PI Denefle P, Rosier M, Arnould-Requigne I, Duverger N, Cambien F;

XX XX Claim 4; Page 109; 297pp; French.

XX DR WPI; 2002-435691/46.

XX XX New polymorphisms in the human ABC1 gene, useful for diagnosing

PT predisposition to myocardial infarct and other cardiovascular diseases.

XX XX CC The present sequence is the human ATP-binding cassette (ABC1)

CC PT transporter gene promoter. This sequence can be used for diagnosing

CC predisposition to diseases associated with the plasma level of high

CC density lipoprotein (HDL) cholesterol, especially familial HDL deficiency

## ALIGNMENTS

20	2891.4	99.9	2893	6 ABN9143	Abn9143 Polymorph
21	2881	99.6	2895	6 ABN9446	Abn9446 Polymorph
22	2875	99.4	2889	6 ABN9349	Abn9349 Polymorph
23	2873	99.3	2888	6 ABN9355	Abn9355 Polymorph
24	2873	99.3	2903	6 ABN9337	Abn9337 Polymorph
25	2865	99.0	2884	6 ABN9350	Abn9350 Polymorph
26	2790.2	96.4	183999	4 AAF9231	Aaf9231 Human ABC
27	1027.8	96.4	183999	13 ADU76470	Adu76470 Human ABC
c	28	2783.6	96.2	21000	13 ADT77194 Type II,d
c	29	2411.4	83.4	2893	6 ABN9338
c	30	1435	49.6	149034	11 ADP65433
c	31	1394.4	48.2	1643	4 AAF24631
c	32	1394.4	48.2	1643	4 AAF24703
c	33	1027.8	35.5	6 ABL58400	Ab158400 Human lar
c	34	889.4	30.7	1033	8 ACC4904
c	35	857.8	29.7	1115	8 ACC49021
c	36	612.2	21.2	900	12 ADJ77895
c	37	612.2	21.2	900	12 ADJ77895
c	38	377.6	13.1	166043	12 ADL08127
c	39	350.4	12.1	7954	12 ADQ97764
c	40	336.4	11.6	151909	14 AEB96535
c	41	333	11.5	80928	12 ADO25290
c	42	330.8	11.4	20645	4 AOL05555
c	43	330.8	11.4	20645	4 ABL98224
c	44	330.6	11.4	5076	5 ABA16599
c	45	328.8	11.4	118788	12 ADP80536

Result	No.	Score	Query	Match	Length	DB	ID	Description
c	1	324	11.2	3004	4	CR857583	CR857583 Pongo pygmaeus	
c	2	322.2	11.1	3004	4	CR857583	CR857583 Pongo pygmaeus	
c	3	285.4	9.9	3127	4	CR860188	CR860188 Pongo pygmaeus	
c	4	275.6	9.5	4503	4	CR858665	CR858665 Pongo pygmaeus	
c	5	267	9.2	1122	4	AY927481	AY927481 Homo sapiens	
c	6	247.6	8.6	3127	4	CR860188	CR860188 Pongo pygmaeus	
c	7	247.2	8.5	3178	4	HSMB03719	AL832411 Homo sapiens	
c	8	239.6	8.3	4503	4	CR858665	CR858665 Pongo pygmaeus	
c	9	237.8	8.2	289	1	AW748338	AW748338 Pongo pygmaeus	
c	10	234.4	8.1	1741	4	CR603303	CR603303 Full1-leng	
c	11	233	8.1	770	9	B2612146	B2612146 WHACLS5TF	
c	12	231.2	8.0	1047	5	BX380958	BX380958 Pongo pygmaeus	
c	13	221.2	7.6	457	1	AW816516	AW816516 QV0-ST023	
c	14	220.6	7.6	696	5	BG616112	BG616112 UT-H-DFO-	
c	15	220.2	7.6	520	4	CR936634	CR936634 Homo sapiens	
c	16	219.4	7.6	577	9	AC265389	AC265389 C1TB1-B1-	
c	17	218.6	7.6	544	9	AC418551	AC418551 RPCI-11-2	
c	18	217.8	7.5	2403	4	BC035989	BC035989 Homo sapiens	
c	19	217	7.5	350	7	CN068016	CN068016 170005318	
c	20	217	7.5	620	5	BQ775487	BQ775487 UT-H-FMO-	
c	21	216.4	7.5	990	3	BW803650	BW803650 AGENCOURT	
c	22	216.2	7.5	467	5	BUT35183	BUT35183 UT-E-DMO-	

GenCore version 5.1.7  
 Copyright (c) 1993 - 2006 Biocceleration Ltd.

## OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 19:02:01 ; Search time 1646.48 Seconds

14529.947 Million Cell updates/sec (without alignments)

Title: US-09-846-456A-3  
 Perfect score: 2893  
 Sequence: 1 acaggccatggggcagggtg.....ctagtcccgccaaaaaccc 2893  
 Scoring table: IDENTITY\_NUC Gapext 1.0  
 Searched: 9793542 seqs, 4134689005 residues  
 Total number of hits satisfying chosen parameters: 19587084  
 Minimum DB seq length: 0  
 Maximum DB seq length: 20000000000  
 Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published Applications NA Main:\*  
 1: /cgn2\_5/ptodata/1/pubpna/us09\_pUBCOMB.seq:/\*  
 2: /cgn2\_6/ptodata/1/pubpna/us08\_pUBCOMB.seq:/\*  
 3: /cgn2\_6/ptodata/1/pubpna/us09\_pUBCOMB.seq:/\*  
 4: /cgn2\_6/ptodata/1/pubpna/us09B\_pUBCOMB.seq:/\*  
 5: /cgn2\_6/ptodata/1/pubpna/us10\_pUBCOMB.seq:/\*  
 6: /cgn2\_6/ptodata/1/pubpna/us10B\_pUBCOMB.seq:/\*  
 7: /cgn2\_6/ptodata/1/pubpna/us10C\_pUBCOMB.seq:/\*  
 8: /cgn2\_6/ptodata/1/pubpna/us10E\_pUBCOMB.seq:/\*  
 9: /cgn2\_6/ptodata/1/pubpna/us10E\_pUBCOMB.seq:/\*  
 10: /cgn2\_6/ptodata/1/pubpna/us11\_pUBCOMB.seq:/\*

RESULT<sup>1</sup>  
 US-09-846-456-3  
 ; Sequence 3, Application US/09846456  
 ; Patent No. US20020146792A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosier, Marie  
 ; APPLICANT: Prades, Catherine  
 ; APPLICANT: Lemoine, Cendrine  
 ; APPLICANT: Naudin, Laurent  
 ; APPLICANT: Denefle, Patrice  
 ; APPLICANT: Duverger, Nicolas  
 ; APPLICANT: Brewyer, Bryan  
 ; APPLICANT: Remaley, Alan  
 ; APPLICANT: Pojo, Silvia  
 ; TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying  
 ; TITLE OF INVENTION: Activity and Therapeutic Uses  
 ; CURRENT APPLICATION NUMBER: US/09/846,456  
 ; PRIORITY APPLICATION NUMBER: US 60/201,280  
 ; FILE REFERENCE: 306.055  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 3  
 ; LENGTH: 2893  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-846-456-3

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2893	100.0	2893	3 US-09-846-456-3	Sequence 3, Appli
2	2893	100.0	2893	3 US-09-94-827-23	Sequence 23, Appli
3	2893	100.0	3231	3 US-09-94-826-1	Sequence 1, Appli
4	2893	100.0	3231	3 US-09-94-827-3	Sequence 3, Appli
5	2891.4	99.9	2893	3 US-09-94-827-137	Sequence 137, Appli
6	2891.4	99.9	2893	3 US-09-94-827-139	Sequence 139, Appli
7	2891.4	99.9	2893	3 US-09-94-827-140	Sequence 140, Appli
8	2891.4	99.9	2893	3 US-09-94-827-141	Sequence 141, Appli
9	2891.4	99.9	2893	3 US-09-94-827-142	Sequence 142, Appli
10	2891.4	99.9	2893	3 US-09-94-827-143	Sequence 143, Appli
11	2891.4	99.9	2893	3 US-09-94-827-144	Sequence 144, Appli
12	2891.4	99.9	2893	3 US-09-94-827-145	Sequence 145, Appli
13	2891.4	99.9	2893	3 US-09-94-827-146	Sequence 146, Appli
14	2891.4	99.9	2893	3 US-09-94-827-148	Sequence 148, Appli
15	2891.4	99.9	2893	3 US-09-94-827-149	Sequence 149, Appli
16	2891.4	99.9	2893	3 US-09-94-827-152	Sequence 152, Appli
17	2891.4	99.9	2893	3 US-09-94-827-153	Sequence 153, Appli
18	2891.4	99.9	2893	3 US-09-94-827-154	Sequence 154, Appli
19	2891.4	99.9	2893	3 US-09-94-827-155	Sequence 155, Appli
20	2891.4	99.9	2893	3 US-09-94-827-157	Sequence 157, Appli
21	2881.4	99.9	2893	3 US-09-94-827-158	Sequence 158, Appli
22	2881	99.6	2893	3 US-09-94-827-147	Sequence 147, Appli
23	2875	99.4	2889	3 US-09-94-827-150	Sequence 150, Appli

## ALIGNMENTS

24 2873 99.3 2888 3 US-09-984-827-156  
 25 2873 99.3 2903 3 US-09-984-827-158  
 26 2865 99.0 2884 3 US-09-984-827-151  
 27 2842 98.2 159138 8 US-10-719-993-5777  
 28 2842 98.2 159138 8 US-10-741-600-17613  
 29 2790.2 96.4 183999 8 US-10-745-377-113-1  
 30 2790.2 96.4 183999 8 US-10-872-113-1  
 31 49.6 149034 9 US-10-287-436A-956  
 32 1394.4 48.2 1643 8 US-10-920-989-3  
 33 1394.4 48.2 1643 9 US-10-972-836-3  
 c 34 377.6 13.1 166043 7 US-10-235-172A-46  
 35 330.8 11.4 20645 3 US-09-764-891-843  
 c 36 327 11.3 141121 8 US-10-741-600-17651  
 37 326.6 11.3 8577 6 US-10-225-567A-675  
 c 38 326.6 11.3 42547 6 US-10-268-822-12  
 c 39 323.8 11.2 53779 9 US-10-737-082-85  
 c 40 323.8 11.2 53779 9 US-10-765-790-85  
 41 323.6 11.2 130244 9 US-10-461-862-104  
 42 322.6 11.1 141121 8 US-10-741-600-17651  
 43 322 11.1 148935 8 US-10-741-600-17708  
 c 44 321.8 11.1 27509 8 US-10-741-600-17735  
 45 321.6 11.1 44063 7 US-10-322-281-718  
 Sequence 718, App

Result No.	Score	Query Match	Length	DB ID	Description
1	2844.8	98.3	159138	7	US-10-995-561-13230
c	2	334.8	11.1	169725	11
c	3	334.4	11.6	189539	11
c	4	330.4	11.4	189539	11
c	5	330	11.4	305312	7
c	6	327.8	11.3	141121	7
c	7	322.6	11.2	92600	7
c	8	322.2	11.1	141121	7
c	9	322	11.1	148935	11
c	10	321.8	11.1	27509	7
c	11	321.4	11.1	100001	11
c	12	321.4	11.1	100001	11
c	13	321	11.1	79528	7
c	14	318.8	11.0	51917	7
c	15	317.2	11.0	161994	11
c	16	314.2	10.9	159695	11
c	17	314	10.9	135019	7
c	18	307.2	10.6	79528	7
c	19	307.2	10.6	86081	7
c	20	306.4	10.6	199321	11
c	21	306	10.6	86950	7
c	22	305.8	10.6	108000	7
c	23	305.8	10.6	108000	7
c	24	305.8	10.6	108000	7
c	25	305.8	10.6	108000	7
c	26	305.8	10.6	108000	7
c	27	305.8	10.6	108000	7
c	28	305.8	10.6	108000	7
c	29	305.8	10.6	108000	7
c	30	305.8	10.6	108000	7
c	31	305.8	10.6	108000	7
c	32	305.8	10.6	108000	7
c	33	305.8	10.6	108000	7
c	34	303.8	10.5	161874	11
c	35	303.2	10.5	149419	11
c	36	303.2	10.5	161726	11
c	37	303.2	10.5	161726	11
c	38	303.2	10.5	166111	11
c	39	303	10.5	175023	11
c	40	302.6	10.5	135019	7
c	41	302.4	10.5	175416	11
c	42	302	10.4	67088	7
c	43	302	10.4	160226	11
c	44	301.4	10.4	163857	11
c	45	300.6	10.4	215308	11

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 19:02:01 ; Search time 203.178 Seconds

Perfect score: 357 (without alignments)

Sequence: 14529.947 Million cell updates/sec

Title: US-09-846-456A-2

Scoring table: IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : Published Applications NA Main: \*  
 1: /cgns\_6/picodata/1/pubnpna/US07\_PUBCOMB.seq: \*  
 2: /cgns\_6/picodata/1/pubnpna/US08\_PUBCOMB.seq: \*  
 3: /cgns\_6/picodata/1/pubnpna/US09\_PUBCOMB.seq: \*  
 4: /cgns\_6/picodata/1/pubnpna/US09B\_PUBCOMB.seq: \*  
 5: /cgns\_6/picodata/1/pubnpna/US10A\_PUBCOMB.seq: \*  
 6: /cgns\_6/picodata/1/pubnpna/US10B\_PUBCOMB.seq: \*  
 7: /cgns\_6/picodata/1/pubnpna/US10C\_PUBCOMB.seq: \*  
 8: /cgns\_6/picodata/1/pubnpna/US10D\_PUBCOMB.seq: \*  
 9: /cgns\_6/picodata/1/pubnpna/US10E\_PUBCOMB.seq: \*  
 10: /cgns\_6/picodata/1/pubnpna/US11\_PUBCOMB.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	357	100.0	357	3	US-09-846-456-2	Sequence 2, Appli
2	357	100.0	357	3	US-09-846-456-2	Sequence 4, Appli
3	353.8	99.1	149034	9	US-10-287-436A-956	Sequence 5, Appli
4	351.2	98.4	183999	7	US-10-745-377-1	Sequence 1, Appli
5	351.2	98.4	183999	8	US-10-872-113-1	Sequence 1, Appli
6	341.4	95.6	159338	8	US-10-719-993-6777	Sequence 6777, Ap
7	341.4	95.6	159338	8	US-10-741-600-17613	Sequence 17613, A
8	340.2	95.3	10345	6	US-10-452-51-14	Sequence 14, Appli
9	340.2	95.3	10345	7	US-10-617-33-14	Sequence 14, Appli
10	340.2	95.3	10345	7	US-10-744-467-14	Sequence 14, Appli
11	340.2	95.3	10345	8	US-10-833-679-14	Sequence 14, Appli
12	340.2	95.3	10345	9	US-10-886-279-14	Sequence 14, Appli
13	203.8	95.1	1062	6	US-10-154-678-101	Sequence 101, Appli
14	203.8	95.1	1062	3	US-0-94-340-101	Sequence 101, Appli
15	203.8	95.1	1062	3	US-0-92-098B-101	Sequence 101, Appli
16	203.8	95.1	1062	3	US-09-995-570-101	Sequence 101, Appli
17	203.8	95.1	1062	5	US-10-000-89-101	Sequence 101, Appli
18	203.8	95.1	1062	5	US-10-000-986-101	Sequence 101, Appli
19	203.8	95.1	1062	6	US-10-154-678-101	Sequence 101, Appli
20	203.8	95.1	1062	6	US-10-001-142-101	Sequence 101, Appli
21	186.4	52.2	201	8	US-10-719-993-10219	Sequence 10219, A
22	186.4	52.2	201	8	US-10-741-600-27232	Sequence 27292, A

#### RESULT 1

US-09-846-456-2

Sequence 2, Application US/09846456  
 Patent No. US20020146792A1  
 GENERAL INFORMATION:  
 / APPLICANT: Rosier, Marie  
 / APPLICANT: Prades, Catherine.  
 / APPLICANT: Lemine, Cendrine  
 / APPLICANT: Naudin, Laurent  
 / APPLICANT: Denefle, Patrice  
 / APPLICANT: Duverger, Nicolas  
 / APPLICANT: Brewer, Bryan  
 / APPLICANT: Remaley, Alan  
 / APPLICANT: Poto, Silvia  
 / TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying  
 / TITLE OF INVENTION: Activity and Therapeutic Uses  
 / CURRENT FILING DATE: 2001-05-02  
 / PRIOR FILING DATE: 2000-05-02  
 / NUMBER OF SEQ ID NOS: 20  
 / SOFTWARE: PatentIn version 3.0  
 / SEQ ID NO: 2  
 / LENGTH: 357  
 / TYPE: DNA  
 / ORGANISM: Homo sapiens  
 US-09-846-456-2

Query Match 100.0%; Score 357; DB 3; Length 357;  
 Best Local Similarity 100.0%; Pred. No. 3 se-105; Mismatches 0; Indels 0; Gaps 0;  
 Matches 357; Conservative 0;  
 FILE REFERENCE: 3806..0505  
 CURRENT APPLICATION NUMBER: US/09/456,456  
 PRIORITY FILING DATE: 2000-05-02  
 NUMBER OF SEQ ID NOS: 20  
 SOFTWARE: PatentIn version 3.0  
 / SEQ ID NO: 2  
 / LENGTH: 357  
 / TYPE: DNA  
 / ORGANISM: Homo sapiens  
 US-09-846-456-2

#### ALIGNMENTS

24	159.4	44.6	10442	8	US-10-920-989-1
25	159.4	44.6	10442	9	US-10-920-989-1
26	159.4	44.6	10442	8	US-10-920-989-1
27	159.4	44.6	10474	8	US-10-920-989-9
28	159.4	44.6	10474	9	US-10-920-989-9
29	159.4	44.6	10474	9	US-10-920-989-9
30	159	44.5	159	3	US-09-846-456-5
31	158.4	44.4	10384	5	US-10-098-939-3
32	158.4	44.4	10423	5	US-10-098-939-3
33	157.4	44.1	159	3	US-09-984-827-16
34	157.4	44.1	10365	5	US-10-098-939-1
35	147	41.2	158	3	US-09-984-827-25
36	147	41.2	1402	8	US-10-719-993-89
37	147	41.2	1402	8	US-10-741-600-197
38	147	41.2	1859	8	US-10-719-993-17
39	147	41.2	1859	8	US-10-741-600-195
40	147	41.2	10405	8	US-10-719-993-100
41	147	41.2	10405	8	US-10-741-600-198
42	146.4	41.0	201	8	US-10-719-993-1710
43	146.4	41.0	201	8	US-10-719-993-1768
44	146.4	41.0	201	8	US-10-719-993-1793
45	146.4	41.0	201	8	US-10-741-600-3805

GenCore version 5.1.7  
 Copyright (c) 1993 - 2006 Biocceleration Ltd.

DNM nucleic - nucleic search, using sw model

run on:	February 8, 2006, 17:12:15 ; Search time 148.123 Seconds (without alignments) 16062.998 Million cell updates/sec
title:	US-09-846-456A-2
perfect score:	357
Sequence:	1 tgggggtctcgatcgaggg.....gagggaaaggaaatgttgtt g 357
scoring table:	IDENTITY_NTC Gapop 10 <sup>-5</sup> , Gapext 1.0
searched:	496997 seqs, 3312346108 residues
total number of hits satisfying chosen parameters:	9993994
minimum DB seq length:	0
maximum DB seq length:	200000000
post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : N Geesect 21 : \*

100

```

1: Geneseqn1990bs:*
2: Geneseqn1990bs:*
3: Geneseqn2000bs:*
4: Geneseqn2001bs:*
5: Geneseqn2001bs:*
6: Geneseqn2002bs:*
7: Geneseqn2002bs:*
8: Geneseqn2003bs:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*
14: Geneseqn2005bs:*

```

הגדה

Result No.	Query	Score	Match	Length	DB	ID
1	357	100.0	357	6	AAD	
2	357	100.0	357	6	ABL	
3	353.8	99.1	149034	11	ADA	
4	351.2	98.4	183999	4	AAF	
5	351.2	98.4	183999	13	ADD	
6	340.2	95.3	10545	3	AAC	
7	203.8	57.1	1062	8	ACC	
8	159.4	44.6	10442	4	AAF	
9	159.4	44.6	10442	4	AAF	
10	159.4	44.6	10442	13	AD	
11	159.4	44.6	10442	14	AD	
12	159.4	44.6	10442	14	AE	
13	159.4	44.6	10474	4	AAF	
14	159.4	44.6	10474	4	AAF	
15	159.4	44.6	10474	4	AAF	
16	159.4	44.6	10474	4	AAF	
17	159	44.6	159	6	AAD	
18	158.4	44.4	10422	10	ADD	
19	158.4	44.4	10422	10	ADD	

Prepared. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

GenCore version 5.1.7  
 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 22:47:42 (without alignments)  
 3382.690 Million cell updates/sec

Title: US-09-846-456A-2

Perfect score: 357

Sequence: 1 tgagggtctcagttgagg... .gagggaaggaaactgttgtg 357

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 6240305 seqs, 449581930 residues

Total number of hits satisfying chosen parameters: 12480610

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%  
 Maximum Match 100%  
 Listing First 45 summaries

Database : Published Applications NA\_New:\*

1: /cgmn\_6/picdata/1/pubpna/US08\_NEW\_PUB.seq;\*  
 2: /cgmn\_6/picdata/1/pubpna/US06\_NEW\_PUB.seq;\*  
 3: /cgmn\_6/picdata/1/pubpna/US07\_NEW\_PUB.seq;\*  
 4: /cgmn\_6/picdata/1/pubpna/PCT\_NEW\_PUB.seq;\*  
 5: /cgmn\_6/picdata/1/pubpna/US05\_NEW\_PUB.seq;\*  
 6: /cgmn\_6/picdata/1/pubpna/US10\_NEW\_PUB.seq;\*  
 7: /cgmn\_6/picdata/1/pubpna/US10\_NEW\_PUB.seq;\*  
 8: /cgmn\_6/picdata/1/pubpna/US11\_NEW\_PUB.seq;\*  
 9: /cgmn\_6/picdata/1/pubpna/US11\_NEW\_PUB.seq;\*  
 10: /cgmn\_6/picdata/1/pubpna/US11\_NEW\_PUB.seq;\*  
 11: /cgmn\_6/picdata/1/pubpna/US11\_NEW\_PUB.seq;\*  
 12: /cgmn\_6/picdata/1/pubpna/US10\_NEW\_PUB.seq;\*

Pred. No. is the number of results predicted by chance  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description	
1	341	95.5	159138	7	US-10-995-561-13240	Sequence 13230, A	
2	186.4	52.2	201	7	US-10-995-561-23994	Sequence 23954, A	
3	155.6	43.6	201	7	US-10-995-561-24507	Sequence 24507, A	
4	147	41.2	1402	7	US-10-995-561-85	Sequence 85, Appl	
5	147	41.2	1859	7	US-10-995-561-84	Sequence 84, Appl	
6	147	41.2	10405	7	US-10-995-561-83	Sequence 83, Appl	
7	146.4	41.0	201	7	US-10-995-561-3388	Sequence 3388, Ap	
8	146.4	41.0	201	7	US-10-995-561-3411	Sequence 3411, Ap	
9	146.4	41.0	201	7	US-10-995-561-3429	Sequence 3429, Ap	
10	145.8	40.8	10412	11	US-11-095-309A-7	Sequence 7, Appl	
11	65	18.2	6786	11	US-11-095-309A-8	Sequence 8, Appl	
12	56	15.7	201	7	US-10-995-561-24209	Sequence 24209, A	
13	44	12.3	201	7	US-10-995-561-24210	Sequence 24210, A	
14	37.8	10.6	168516	11	US-11-095-32881	Sequence 3, Appl	
15	34.6	9.7	6768	11	US-11-093-889-1	Sequence 1, Appl	
c	16	33.6	9.4	600	11	US-11-136-527-7814	Sequence 7814, Ap
c	17	33.6	9.4	2412	11	US-11-136-527-3714	Sequence 3714, Ap
c	18	33.4	9.4	1598	7	US-10-750-185-32881	Sequence 32881, A
c	19	33.4	9.4	1598	7	US-10-750-623-32881	Sequence 32881, A
c	20	33.2	9.3	6412	11	US-11-093-889-3	Sequence 3, Appl
c	21	33	9.2	18238	7	US-10-995-561-13386	Sequence 13386, A

Sequence 123, Appl  
 Sequence 42, Appl  
 Sequence 43, Appl  
 Sequence 41, Appl  
 Sequence 74, Appl  
 Sequence 85, Appl  
 Sequence 53588, A  
 Sequence 53588, A  
 Sequence 5010, Appl  
 Sequence 5015, Appl  
 Sequence 6778, Appl  
 Sequence 2642, Appl  
 Sequence 152, Appl  
 Sequence 2859, Appl  
 Sequence 13212, A  
 Sequence 32457, A  
 Sequence 56717, A  
 Sequence 56717, A  
 Sequence 13259, A  
 Sequence 13259, A  
 Sequence 48, Appl  
 Sequence 79, Appl  
 Sequence 78, Appl  
 Sequence 13233, A

ALIGNMENTS

RESULT 1  
 US-10-995-561-13230  
 ; Sequence 13230, Application US/10995561  
 ; Publication No. US20050272054A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CARGILL, Michael et al.  
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF DETECTION AND USES THEREOF  
 ; TITLE OF INVENTION: FILE REFERENCE: CL001559  
 ; CURRENT APPLICATION NUMBER: US/10/995,561  
 ; CURRENT FILING DATE: 2005-11-24  
 ; NUMBER OF SEQ ID NOS: 85702  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 13230  
 ; LENGTH: 159138  
 ; TYPE: DNA  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)...(159138)  
 ; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables US-10-995-561-13230

## ALIGNMENTS

RESULT 1

LOCUS AX351030 Sequence 2 from Patent WO013746 .  
DEFINITION AX351030  
ACCESSION AX351030.1 GI:18816386  
VERSION

SOURCE	Homo sapiens (human)
ORGANISM	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarzhini;
	Hominidae; Homo.

**AUTHORS** Rosser-Hontus, M.F., Pridie, C., Lemire, C., Naoum, L., Denarie, F.;  
**TITLE** Regulatory nucleic acid sequences of the abcl gene  
**JOURNAL** Patent: WO 0183746-A 2 08-NOV-2001;

```

FEATURES          location, qualities
Source           1. .357
                  /organism="Homo sapiens"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:9606"

```

Query Match Score 357; DB 6; Length 357;  
Best\_Local\_Similarity 100.0%; Pred. No.: 1.8e-94;

Qy	1	TGGAGGCTCTAGCTGAGGGCTGGATTAGCAGTCCTCATGGTGTATGGCTTTCGACCA	60
Db	1	TGGAGGCTCTAGCTGAGGGCTGGATTAGCAGTCCTCATGGTGTATGGCTTTCGACCA	60
Qy	61	ATAACTCATGGCTTCCCTCTCCCTTAATGTTAATGTTAACAGGCCAGGGT	120
Db	61	ATAACTCATGGCTTCCCTCTCCCTTAATGTTAATGTTAACAGGCCAGGGT	120
Qy	61	CCCTGCTGCTGCTCGCTGGCTGGCTTCCGGACCAAGCTGGCTGGCT	180
Db	61	CCCTGCTGCTGCTCGCTGGCTGGCTTCCGGACCAAGCTGGCTGGCT	180
Qy	121	CCCTGCTGCTGCTCGCTGGCTGGCTTCCGGACCAAGCTGGCTGGCT	180
Db	121	CCCTGCTGCTGCTCGCTGGCTGGCTTCCGGACCAAGCTGGCTGGCT	180

SUMMARY

Sault		Query No.	Score	Match Length	DB ID	Description
1	1	357	100.0	357	6	AX31030 Sequence
1	2	353.8	99.1	149034	8	AF275948 Homo sapi
1	3	351.2	98.4	183919	6	AX02589 Sequence
1	4	340.2	95.3	480	8	HSA252277 Homo sapi
1	5	340.2	95.3	10515	6	AR93492 Sequence
1	6	340.2	95.3	129608	8	AL353685 Human DNA
1	7	340.2	95.3	175004	14	AC012230 Homo sapi
1	8	340.2	95.3	201144	8	AF287262 Homo sapi
1	9	294.2	82.4	183910	14	AC160520 Papio ha
1	10	294.2	82.4	20793	14	AC160521 Papio ha
1	11	292.6	82.0	200940	14	AC161030 Colobus
1	12	285	79.8	183118	14	AC160722 Aotus na
1	13	284	79.6	171939	14	AC160721 Aotus na
1	14	280.8	78.7	198224	14	AC161090 Callicebus
1	15	280.8	78.7	206547	14	AC161097 Saimiri
1	16	271.4	76.0	21470	14	AC160525 Lemur ca
1	17	251.1	70.4	90598	14	AC021345 Homo sap
1	18	231	64.7	179848	14	AC139880 Lemur ca

GenCore version 5.1.7  
(c) 1993 - 2006 Biocceleration Ltd.

Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2006, 15:01:42 ; Search time 997.664 Seconds  
(without alignment)  
16742.09 Million cell updates/sec.

Title: US-09-846-456A-2  
Perfect Score: 357  
Sequence: 1 tggaggtctcagtgagagg.....gaggagaaggaaactgttgtg 357

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listting first 45 summaries

Database : EST.\*  
1: 9b\_est1:\*

2: 9b\_est2:\*

3: 9b\_est3:\*

4: 9b\_nuc:\*

5: 9b\_est4:\*

6: 9b\_est5:\*

7: 9b\_est6:\*

8: 9b\_est7:\*

9: 9b\_gbs1:\*

10: 9b\_gbs2:\*

11: 9b\_gbs3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	169.4	47.5	648	9	BZ865821	BZ865821 CH240_259
2	159.4	44.6	547	3	AL69854	DKP2p616N
3	159.4	44.6	583	3	BP280727	BP280727
4	159.4	44.6	595	3	BP280045	BP280045
5	145.8	40.8	583	3	BP200657	BP200657
6	145.8	40.8	663	5	BX955241	DKP2p781F
7	145.2	40.7	583	3	BP287529	BP287529
8	145.2	40.4	736	1	AU135598	AU135598
9	75.8	21.2	619	2	BB657864	BB657864
10.	75.8.	21.2.	478	4	AK051920	Mus muscu
			24377	2	HSC1ZB081	ZA4377 HSC1ZB081
				2	BC384217	BC384217 303216 MA
				8	DN853427	DN853427 4149571 B
				4	CNSDBXBH	CR645863 Tetraodon
				3	CN901916	BJ901916
				9	CX260141	CX260141 1313535 N
				5	BK911478	BK911478 BX911478
				7	CO927141	CO927141 AGENCOURT
				5	BY175500	BY175500
				8	DN45045	DN45045 MI02C08.3
				10	CNS02D01	MI192682 Tetraodon
				5	BUB67612	BUB67612 MI02C08 P

#### RESULTS

#### 1

#### BZ865821

#### LOCUS

#### DEFINITION

#### CH240\_259B12.TJ CHORI-240

#### genomic survey sequence.

#### ACCESSION

#### BZ865821

#### VERSION

#### GSS.

#### KEYWORDS

#### Bos taurus (cow)

#### ORGANISM

#### Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi;

#### Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

#### Pecora; Bovidae; Bovinae; Bos.

#### REFERENCE

#### AUTHORS

#### zhao,S., Shetty,J., Shatsman,S., Tsugay,G., Geer,K., Shivarbejn,A., Gebregeorgis,E., Chen,D., Riggs,F., de Jong,P., Crawford,A.M. and McEwan,J.C.

#### TITLE

#### JOURNAL

#### COMMENT

#### Unpublished (2003)

#### CONTACT

#### Shaying Zhao

#### Department of Eukaryotic Genomics

#### The Institute for Genomic Research

#### 9712 Medical Center Dr., Rockville, MD 20850, USA

#### Tel: 301 838 0200

#### Fax: 301 838 0208

#### Email: szha@tigr.org

#### Clones are derived from the bovine BAC library CHORI-240

#### (http://www.chori.org/bacpac/bovine240.htm).

#### For BAC library

#### availability, please contact Pieter de Jong (pdejong@mail.cho.org).

#### Clones may be purchased from BACPAC Resources

#### (http://www.chori.org/bacpac/ordering-information.htm).

#### This work

#### was undertaken as part of the International Bovine BAC Mapping

#### Consortium (IBMC) by AgResearch Ltd., New Zealand and The

#### Institute of Genomic Research (TIGR), USA.

#### Plate: 259 row: B column: 12

#### Seq primer: SP6

#### Class: BAC ends.

#### FEATURES

#### source

#### Location/Qualifiers

#### 1 . 648

#### /organism="Bos taurus"

#### /mol\_type="genomic DNA"

#### /strain="Breed: Hereford"

#### /db\_xref="taxon:9913"

#### /clone="CH240\_259B12"

#### /sex="Male"

#### ALIGNMENTS

GenCore version 5.1.7  
 Copyright (c) 1993 - 2006 Bioceleration Ltd.

CM nucleic - nucleic search, using sw model

Run on: February 8, 2006, 23:04:12 ; Search time 11:099.8 Seconds  
 Perfect score: US-09-846-456A-1  
 Sequence: 3231 1 acgggcatgttgttcaggatg.....gcacatccccaccatt 3231

Scoring table: IDENTITY\_NUC Gapov 10.0 , Gapext 1.0

Searched: 5883141 seqs, 2842172563 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100%  
 Listing first 45 summaries

Database : GenEmbl:  
 1: qb\_ba: \*  
 2: qb\_in: \*  
 3: qb\_env: \*  
 4: qb\_om: \*  
 5: qb\_ov: \*  
 6: qb\_pat: \*  
 7: qb\_ph: \*  
 8: qb\_pr: \*  
 9: qb\_ro: \*  
 10: qb\_sts: \*  
 11: qb\_sv: \*  
 12: qb\_un: \*  
 13: qb\_vl: \*  
 14: qb\_ng: \*  
 15: qb\_pl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	3231	100.0	3231	6	AX351029		AX351029 Sequence
2	3177.8	96.8	183999	6	AX092589		AX092589 Sequence
c 3	3121.6	96.6	96717	8	AL359182		AL359182 Human DNA
4	2952.9	91.5	20144	8	AF287262		AF287262 Homo sapi
5	2893	89.5	2893	6	AX351031		AX351031 Sequence
c 6	2254.4	69.8	183930	14	AC160520		AC160520 Papio ham
c 7	2151.4	66.7	200920	14	AC161030		AC161030 Colobus g
8	1773	54.9	149034	8	AF275948		AF275948 Homo sapi
c 9	1642.6	50.8	183118	14	AC160722		AC160722 Aotus nan
10	1571.2	48.6	198224	14	AC161090		AC161090 Callithri
c 11	1570.6	48.6	206547	14	AC161097		AC161097 Callicebu
12	1485.4	46.0	1643	6	AR07251		AR07251 Sequence
13	1485.4	46.0	1643	6	AR628826		AR628826 Sequence
14	1485.4	46.0	1643	6	AX060715		AX060715 Sequence
15	1485.4	46.0	1643	6	AX060894		AX060894 Sequence
16	1261.2	39.0	248297	14	AC160525		AC160525 Saimiri b
17	1227.8	38.0	175064	14	AC012230		AC012230 Homo sapi
18	1134.8	35.1	1197	6	AR575615		AR575615 Sequence

## ALIGNMENTS

RESULT 1  
 AX351029 LOCUS Sequence 1 From Patent WO01837476. 3231 bp DNA linear PAT 06-FEB-2002  
 DEFINITION AX351029 AC005837 Human DNA  
 ACCESSION AX351029 GI:18616385 AP003357 Homo sapi  
 VERSIONS AC087826 Homo sapi AL117381 Human DNA  
 KEYWORDS AL034400 Human DNA AC024101 Homo sapi AC146385 Pan trogl  
 AC016898 Homo sapi AC021345 Homo sapi AC021345 Homo sapi  
 AC016898 Homo sapi AC016898 Homo sapi AC016898 Homo sapi  
 AC010624 Homo sapi AC010624 Homo sapi AC010624 Homo sapi  
 AP003357 Homo sapi AP003357 Homo sapi AP003357 Homo sapi  
 AC005837 Human DNA AC005837 Human DNA AC005837 Human DNA  
 AC005837 Human DNA AC005837 Human DNA AC005837 Human DNA  
 AL592309 Human DNA AL592309 Human DNA AL592309 Human DNA  
 AL355226 Human DNA AL355226 Human DNA AL355226 Human DNA  
 AC013445 Homo sapi AC013445 Homo sapi AC013445 Homo sapi  
 AL034400 Human DNA HS198221 HS198221 HS198221

## REFERENCE

AUTHORS Rosier-Montus, M.F., Prades C., Lemire, C., Naudin, L., Denefle, P., Brewer, B., Duverger, N., Remaley, A. and Santamina-Pojo, S.  
 TITLE Regulatory nucleic acid sequences of the abcl gene  
 JOURNAL Patent: WO 01837476-A 1 08-NOV-2001;  
 FEATURES Source Aventis Pharma S.A. (FR)  
 ORIGIN Location/Qualifiers 1. .3231  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

## ORIGIN

Query Match 100.0%; Score 3231; DB 6; Length 3231;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 ACAGGGCATGGCAGGTCCTGAATCTCACTTACTCGGGAGGTGGCAATGA 60  
 Db 1 ACAGGCATGGCAGGTCCTGAATCTCACTTACTCGGGAGGTGGCAATGA 60  
 Qy 61 GCCAGATCGACATGACTCGACTCCGCTGGCACAAANGTGAAACTCCATT 120  
 Db 61 GCCAGATCGACATGACTCGACTCCGCTGGCACAAANGTGAAACTCCATT 120  
 Qy 61 GCCAGATCGACATGACTCGACTCCGCTGGCACAAANGTGAAACTCCATT 120

## SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	3231	100.0	3231	6	AX351029		AX351029 Sequence
2	3177.8	96.8	183999	6	AX092589		AX092589 Sequence
c 3	3121.6	96.6	96717	8	AL359182		AL359182 Human DNA
4	2952.9	91.5	20144	8	AF287262		AF287262 Homo sapi
5	2893	89.5	2893	6	AX351031		AX351031 Sequence
c 6	2254.4	69.8	183930	14	AC160520		AC160520 Papio ham
c 7	2151.4	66.7	200920	14	AC161030		AC161030 Colobus g
8	1773	54.9	149034	8	AF275948		AF275948 Homo sapi
c 9	1642.6	50.8	183118	14	AC160722		AC160722 Aotus nan
10	1571.2	48.6	198224	14	AC161090		AC161090 Callithri
c 11	1570.6	48.6	206547	14	AC161097		AC161097 Callicebu
12	1485.4	46.0	1643	6	AR07251		AR07251 Sequence
13	1485.4	46.0	1643	6	AR628826		AR628826 Sequence
14	1485.4	46.0	1643	6	AX060715		AX060715 Sequence
15	1485.4	46.0	1643	6	AX060894		AX060894 Sequence
16	1261.2	39.0	248297	14	AC160525		AC160525 Saimiri b
17	1227.8	38.0	175064	14	AC012230		AC012230 Homo sapi
18	1134.8	35.1	1197	6	AR575615		AR575615 Sequence

Result No.	Score	Query Match	Length	DB ID	Description
1	336	10.4	763	AU121731	AU121731 AU121731
c	2	324	10.0	3004	CR857583 Pongo pyg
c	3	322	10.0	3004	CR857583 Pongo pyg
c	4	314.4	9.7	663	BX955241 DKF2P81F CR860188 Pongo pyg
c	5	295.4	8.8	3127	CR860188 Pongo pyg
c	6	275.6	8.5	4503	CR858665 Pongo pyg
c	7	267	8.3	1122	AY927481 Pongo pyg
c	8	247.6	7.7	3127	CR860188 Pongo pyg
c	9	247	7.7	3127	CR860188 Pongo pyg
c	10	239.6	7.4	4503	CR858665 Pongo pyg
c	11	237.8	7.4	289	AW748338 CR6-BT025
c	12	234.4	7.3	1741	CR8603303 full1-leng
c	13	233	7.2	770	BZ612146 WFLCL5TF
c	14	231.2	7.2	1047	BX380958 BX380958
c	15	223.4	6.9	583	BZ287529 BZ287529
c	16	221.8	6.9	736	AU135588 AU135588
c	17	221.4	6.9	583	BP200657 BP200657
c	18	221.4	6.9	583	BP280727 BP280727
c	19	221.4	6.9	595	BP280045 BP280045
c	20	221.2	6.8	457	AW161516 QV0-ST023
c	21	220.6	6.8	696	BG616112 UI-H-DFO-
c	22	220.2	6.8	5920	CR936634 Homo sapi

ALIGNMENTS

```

RESULT 1
AAD37265
ID AAD37265 standard; DNA; 3231 BP.
XX
XX
AC
AC
XX
DT 21-AUG-2002 (first entry)
XX
XX
DE Human ABC1 transcription regulatory DNA #1.
XX
KW Human; ATP-binding cassette 1; ABC1 gene regulation; atherosclerosis;
cholesterol metabolism; hypercholesterolaemia; antisense therapy; ds-
XX
OS Homo sapiens.

```

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. No. is derived by analysis of the total score distribution.

SUMMARY

built	No.	Query			Length	DB	ID	Description
		Score	Match	Start				
1	3231	100.0	3231	6	AAD37265	Human	ABC	Aad37265 Human ABC
2	3231	100.0	3231	6	ABU58147	Human	ABC	Abf58147 Human ABC
3	3121.8	96.8	18399	4	AAR92831	Human	ABC	Aaf92831 Human ABC
4	3117.8	96.8	18399	13	ADU76470	Human	ABC	Adu76470 Human ABC
5	3121.6	96.6	21000	13	ADT77194	Type II C	ABC	Adt77194 Type II C
6	2910	90.1	2910	6	AAD37267	Human	ABC	Aad37267 Human ABC
7	2893	89.5	2893	6	ABR92322	Human	ABC	Abn92322 Human ABC
8	2891.4	89.5	2893	6	ABN93556	Polymorph	ABC	Abn93556 Polymorph
9	2891.4	89.5	2893	6	ABN9342	Polymorph	ABC	Abn9342 Polymorph
10	2891.4	89.5	2893	6	ABN9354	Polymorph	ABC	Abn9354 Polymorph
11	2891.4	89.5	2893	6	ABN9340	Polymorph	ABC	Abn9340 Polymorph
12	2891.4	89.5	2893	6	ABN9345	Polymorph	ABC	Abn9345 Polymorph
13	2891.4	89.5	2893	6	ABN9347	Polymorph	ABC	Abn9347 Polymorph
14	2891.4	89.5	2893	6	ABN9336	Polymorph	ABC	Abn9336 Polymorph
15	2891.4	89.5	2893	6	ABN9339	Polymorph	ABC	Abn9339 Polymorph
16	2891.4	89.5	2893	6	ABN9352	Polymorph	ABC	Abn9352 Polymorph
17	2891.4	89.5	2893	6	ABN9341	Polymorph	ABC	Abn9341 Polymorph
18	2891.4	89.5	2893	6	ABN9348	Polymorph	ABC	Abn9348 Polymorph
19	2891.4	89.5	2893	6	ABN9357	Polymorph	ABC	Abn9357 Polymorph

卷之三

GenCore version 5.1.7  
 Copyright (c) 1993 - 2006 Biocceleration Ltd.  
 MM nucleic - nucleic search, using SW model  
 run on: February 10, 2006, 22:47:42 ; Search time 858.843 Seconds  
 (without alignments)  
 3382.690 Million cell updates/sec  
 title: US-09-846-456A-1.  
 perfect score: 3231  
 sequence: 1 acaggccatggcggagggt.....gccccacatecccacacctt 3231  
 scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0  
 searched: 6240305 seqs, 449581130 residues  
 total number of hits satisfying chosen parameters:  
 12480610  
 minimum DB seq length: 0  
 maximum DB seq length: 2000000000  
 post-processing: Minimum Match 0%  
 Maximum Match 100%

```

Published Applications NA_New :*
 1: /cgn2_6/_ptodata/1/pubnra/us08_NEW_PUB_seq:*
 2: /cgn2_6/_ptodata/1/pubnra/us16_NEW_PUB_seq:*
 3: /cgn2_6/_ptodata/1/pubnra/us77_NEW_PUB_seq:*
 4: /cgn2_6/_ptodata/1/pubnra/PCT_NEW_PUB_seq:*
 5: /cgn2_6/_ptodata/1/pubnra/us59_NEW_PUB_seq:*
 6: /cgn2_6/_ptodata/1/pubnra/us10_NEW_PUB_seq:*
 7: /cgn2_6/_ptodata/1/pubnra/us10_NEW_PUB_seq:*
 8: /cgn2_6/_ptodata/1/pubnra/us11_NEW_PUB_seq:*
 9: /cgn2_6/_ptodata/1/pubnra/us11_NEW_PUB_seq:*
10: /cgn2_6/_ptodata/1/pubnra/us11_NEW_PUB_seq:*
11: /cgn2_6/_ptodata/1/pubnra/us11_NEW_PUB_seq:*
12: /cgn2_6/_ptodata/1/pubnra/us60_NEW_PUB_seq:*

```

red. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result	Query No.	Score	Match	Length	DB ID	Description
--------	-----------	-------	-------	--------	-------	-------------



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 06:52:37 ; Search time 20.1384 Seconds  
(without alignments)  
14034.494 Million cell updates/sec

Title: US-09-846-456A-5  
Perfect score: 159  
Sequence: 1 ttaatgaccaggcacggcg.....ctttcagaagaagacaaca 159

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:  
 1: /cgn2\_6/picodata/1/in/a/1 COMB.seq:  
 2: /cgn2\_6/picodata/1/in/a/5\_-COMB.seq:  
 3: /cgn2\_6/picodata/1/in/a/6A COMB.seq:  
 4: /cgn2\_6/picodata/1/in/a/6B COMB.seq:  
 5: /cgn2\_6/picodata/1/in/a/H COMB.seq:  
 6: /cgn2\_6/picodata/1/in/a/PCTUS\_COMB.seq:  
 7: /cgn2\_6/picodata/1/in/a/PP COMB.seq:  
 8: /cgn2\_6/picodata/1/in/a/R\_-COMB.seq:  
 9: /cgn2\_6/picodata/1/in/a/backfile1.seq:  
 \*

RESULT 1  
US-09-596-141C-1

/ Sequence 1, Application US/09596141C  
 / Patent No. 6821174  
 / GENERAL INFORMATION:  
 / APPLICANT: Lawn, Richard M.  
 / APPLICANT: Wade, David  
 / APPLICANT: Oran, John F.  
 / APPLICANT: Garvin, Michael  
 / TITLE OF INVENTION: Compositions and Methods for Increasing Cholesterol Efflux and Raising HDL using ATP Binding Cassette Transporter Protein ABC1.  
 / TITLE OF INVENTION: Transporter Protein ABC1.  
 / FILE REFERENCE: 99\_395-B  
 / CURRENT APPLICATION NUMBER: US/09/596,141C  
 / PRIORITY FILING DATE: 2000-06-16  
 / PRIOR APPLICATION NUMBER: US 60/140,264  
 / PRIORITY FILING DATE: 1999-06-18  
 / PRIOR APPLICATION NUMBER: US 60/153,872  
 / PRIORITY FILING DATE: 1999-09-14  
 / PRIORITY FILING DATE: 1999-11-19  
 / NUMBER OF SEQ ID NOS: 62  
 / SEQ ID NO 1

Length 10442  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1)..(10442)  
OTHER INFORMATION: All n's are unknown.  
US-09-596-141C-1

Query Match Score 155.8; Score 155.8; DB 3; Length 10442;  
Best Local Similarity 98.7%; Pred. No. 8.6e-38;  
Matches 157; Conservatve 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTATGACCAGGCCAGGGCCTCCCTGCTTCAGGCTCTGGCGCCCTCAGGCTCC 60  
Db 198 TTATGACCAGGCCAGGGCCTCCCTGCTTCAGGCTCTGGCGCCCTCAGGCTCC 257

Description

Result No.	Query	Match	Length	DB	ID
1	155.8	98.0	10442	3	US-09-596-141C-1
2	155.8	98.0	10442	3	US-09-555-522C-1
3	155.8	98.0	10442	3	US-09-596-141C-7
4	155.8	98.0	10474	3	US-09-556-141C-9
5	155.8	98.0	10474	3	US-09-555-522C-7
6	155.8	98.0	10474	3	US-09-555-522C-9
7	142.2	89.4	447	3	US-09-621-976-13889
8	142.2	89.4	1062	3	US-10-000-483-101
9	142.2	89.4	10545	3	US-09-556-192A-14
10	155.8	85.0	10442	3	US-09-556-192A-2
c 11	35.8	22.5	234884	3	US-09-949-016-16420
c 12	35	22.0	298	3	US-09-513-999C-10257
c 13	34.6	21.8	8920	3	US-09-949-016-15145
c 14	34.6	21.8	30678	3	US-09-949-016-12838
c 15	33.2	20.9	6588	3	US-09-949-016-1076
c 16	32.8	20.5	137753	3	US-09-949-016-17434
c 17	32.6	20.5	601	3	US-09-949-016-112405
c 18	32.6	20.5	601	3	US-09-949-016-112406
c 19	32.6	20.5	86380	3	US-09-949-016-14837
c 20	30.6	19.2	2395	3	US-09-949-016-1365
c 21	30.6	19.2	861	3	US-09-949-016-15910
c 22	30.4	19.1	390	3	US-09-513-999C-1013
c 23	30.4	19.1	485	3	US-09-513-999C-1002
c 24	30.4	19.1	532	3	US-09-513-999C-1003

SUMMARIES

%

Result No.	Score	Match	Length	DB	ID
1	155.8	98.0	10442	3	US-09-596-141C-1
2	155.8	98.0	10442	3	US-09-555-522C-1
3	155.8	98.0	10442	3	US-09-596-141C-7
4	155.8	98.0	10474	3	US-09-556-141C-9
5	155.8	98.0	10474	3	US-09-555-522C-7
6	155.8	98.0	10474	3	US-09-555-522C-9
7	142.2	89.4	447	3	US-09-621-976-13889
8	142.2	89.4	1062	3	US-10-000-483-101
9	142.2	89.4	10545	3	US-09-556-192A-14
10	155.8	85.0	10442	3	US-09-556-192A-2
c 11	35.8	22.5	234884	3	US-09-949-016-16420
c 12	35	22.0	298	3	US-09-513-999C-10257
c 13	34.6	21.8	8920	3	US-09-949-016-15145
c 14	34.6	21.8	30678	3	US-09-949-016-12838
c 15	33.2	20.9	6588	3	US-09-949-016-1076
c 16	32.8	20.5	137753	3	US-09-949-016-17434
c 17	32.6	20.5	601	3	US-09-949-016-112405
c 18	32.6	20.5	601	3	US-09-949-016-112406
c 19	32.6	20.5	86380	3	US-09-949-016-14837
c 20	30.6	19.2	2395	3	US-09-949-016-1365
c 21	30.6	19.2	861	3	US-09-949-016-15910
c 22	30.4	19.1	390	3	US-09-513-999C-1013
c 23	30.4	19.1	485	3	US-09-513-999C-1002
c 24	30.4	19.1	532	3	US-09-513-999C-1003

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using SW model

Run on: February 10, 2006, 06:52:37 ; Search time 45.2164 Seconds  
(without alignments)  
14034.494 Million cell updates/sec

Title: US-09-846-456A-2  
Perfect score: 357  
Sequence: 1 tggaggctcaggtgagagg.....gagggaaaggaaagtgttg 357

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 130357 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:  
1: /cgn2\_6/ptodata/1/in/1/COMB.seq:/\*  
2: /cgn2\_6/ptodata/1/in/5/COMB.seq:/\*  
3: /cgn2\_6/ptodata/1/in/6A/COMB.seq:/\*  
4: /cgn2\_6/ptodata/1/in/6B/COMB.seq:/\*  
5: /cgn2\_6/ptodata/1/in/H/COMB.seq:/\*  
6: /cgn2\_6/ptodata/1/in/PICTUS/COMB.seq:/\*  
7: /cgn2\_6/ptodata/1/in/PP/COMB.seq:/\*  
8: /cgn2\_6/ptodata/1/in/RE/COMB.seq:/\*  
9: /cgn2\_6/ptodata/1/in/batchfile1.seq:/\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**RESULTS**

US-09-526-193A-1  
; Sequence 14, Application US/09526193A  
; Patent No. 6617122  
; GENERAL INFORMATION:  
; APPLICANT: Hayden, Michael R.  
; APPLICANT: Brooks-Wilson, Simon N.  
; APPLICANT: Pimstone, Simon N.  
; TITLE OF INVENTION: CHOLESTEROL LEVELS FOR MODULATING  
; FILE REFERENCE: 50110/002005  
; CURRENT FILING DATE: 2000-03-15  
; PRIOR APPLICATION NUMBER: 60/124,702  
; PRIOR FILING DATE: 1999-03-15  
; PRIOR APPLICATION NUMBER: 60/138,048  
; PRIOR FILING DATE: 1999-06-08  
; PRIOR APPLICATION NUMBER: 60/139,600  
; PRIOR FILING DATE: 1999-06-17  
; PRIOR APPLICATION NUMBER: 60/151,977  
; NUMBER OF SEQ ID NOS: 287  
; SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 14

Description

Query Match Score Length DB ID Description

Result No.	Score	Query	Match	Length	DB	ID	Description	
1	340.2	95.3	10545	3	US-09-526-193A-14		Sequence 14, Appli	
2	203.8	57.1	1062	3	US-10-00-489-101		Sequence 101, Appli	
3	203.4	57.0	447	3	US-09-621-976-13889		Sequence 13889, Appli	
4	159.4	44.6	10442	3	US-09-595-526C-1		Sequence 1, Appli	
5	159.4	44.6	10442	3	US-09-595-526C-1		Sequence 1, Appli	
6	159.4	44.6	10474	3	US-09-596-14IC-7		Sequence 7, Appli	
7	159.4	44.6	10474	3	US-09-596-14IC-9		Sequence 9, Appli	
8	159.4	44.6	10474	3	US-09-595-526C-7		Sequence 7, Appli	
9	159.4	44.6	10474	3	US-09-595-526C-9		Sequence 9, Appli	
10	335.8	38.0	7860	3	US-09-526-193A-2		Sequence 2, Appli	
11	37.8	10.6	8920	3	US-09-949-016-15145		Sequence 15145, Appli	
12	37.8	10.6	30678	3	US-09-949-016-12818		Sequence 12818, Appli	
C	13	36.4	10.2	154600	3	US-09-949-016-14757		Sequence 14757, Appli
C	14	35.8	10.0	858	3	US-09-505-236-1287		Sequence 1287, Appli
C	15	35.8	10.0	92407	3	US-09-596-002-3		Sequence 36, Appli
C	16	35.8	10.0	234884	3	US-09-949-016-16420		Sequence 16420, Appli
C	17	35.2	9.9	601	3	US-09-949-016-21645		Sequence 21645, Appli
C	18	35.2	9.9	601	3	US-09-949-016-156690		Sequence 156690, Appli
C	19	35.2	9.9	231129	3	US-09-949-016-16110		Sequence 16110, Appli
C	20	35.2	9.9	266293	3	US-09-949-016-11934		Sequence 11934, Appli
C	21	34.4	9.8	298	3	US-09-513-999C-10457		Sequence 10457, Appli
C	22	34.4	9.6	6588	3	US-09-949-016-1076		Sequence 1076, Appli
C	23	33.4	9.4	4438	3	US-09-949-016-13578		Sequence 13578, Appli
C	24	32.8	9.2	137753	3	US-09-949-016-17404		Sequence 17404, Appli

ALIGNMENTS

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 06:52:37 ; Search time 366.418 Seconds  
(without alignments)  
14034.494 Million cell updates/sec

Title: US-09-846-456A-3  
Perfect score: 2893  
Sequence: 1 acgggcatgttgtcaggatgtg.....ctagtccggcaaaaaacccc 2893

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

1: /cgpn2\_6/pidata/1/ina/1-COMB.seq:\*

2: /cgpn2\_6/pidata/1/ina/5-COMB.seq:\*

3: /cgpn2\_6/pidata/1/ina/6A-COMB.seq:\*

4: /cgpn2\_6/pidata/1/ina/6B-COMB.seq:\*

5: /cgpn2\_6/pidata/1/ina/PCUTS\_COMB.seq:\*

6: /cgpn2\_6/pidata/1/ina/PP-COMB.seq:\*

7: /cgpn2\_6/pidata/1/ina/backfile1.seq:\*

8: /cgpn2\_6/pidata/1/ina/backfile1.seq:\*

9: /cgpn2\_6/pidata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description	
1	1394.4	48.2	1643	3	US-09-56-141C-3	Sequence 3, Appli	
2	1394.4	48.2	1643	3	US-09-59-526C-3	Sequence 3, Appli	
3	1027.8	35.5	1197	3	US-09-56-377-1	Sequence 1, Appli	
4	335.4	12.0	118143	3	US-09-94-016-17196	Sequence 17196, A	
C	5	335.4	11.6	13821	3	US-09-94-016-13690	Sequence 13690, A
C	6	333.3	11.5	84870	3	US-09-94-016-17547	Sequence 17547, A
C	7	330.4	11.4	36148	3	US-09-94-016-12969	Sequence 12969, A
C	8	330	11.4	14519	3	US-09-94-016-15611	Sequence 15611, A
9	330	11.4	14519	3	US-09-94-016-15612	Sequence 15612, A	
10	325.2	11.2	31318	3	US-09-94-016-12495	Sequence 12495, A	
11	325.2	11.2	31319	3	US-09-94-016-15963	Sequence 15963, A	
C	12	324.8	11.2	87734	3	US-09-94-016-17521	Sequence 17521, A
C	13	324.4	11.2	78630	3	US-09-94-016-16790	Sequence 16790, A
C	14	323.4	11.2	44019	3	US-09-94-016-14902	Sequence 14902, A
C	15	321.6	11.1	9208	3	US-09-94-016-15567	Sequence 15567, A
C	16	321.2	11.1	786431	3	US-09-94-016-189-3	Sequence 3, Appli
C	17	319.2	11.0	4441	3	US-09-94-016-15325	Sequence 15325, A
C	18	319	11.0	11543	3	US-09-94-016-12071	Sequence 12071, A
C	19	319	11.0	11543	3	US-09-94-016-12673	Sequence 12673, A
C	20	319	11.0	11543	3	US-09-94-016-16172	Sequence 16172, A
C	21	319	11.0	11544	3	US-09-94-016-16173	Sequence 16173, A
C	22	319	11.0	11544	3	US-09-94-016-16174	Sequence 16174, A
C	23	319	11.0	11544	3	US-09-94-016-16175	Sequence 16175, A
C	24	318.2	11.0	37292	3	US-09-94-016-15382	Sequence 15382, A

## ALIGNMENTS

RESULT 1  
US-09-56-141C-3  
; Sequence 3, Appli Application US/09596141C  
; Patent No. 682174  
; GENERAL INFORMATION:  
; APPLICANT: Lawn, Richard M.  
; APPLICANT: Wade, David M.  
; APPLICANT: Oram, John F.  
; APPLICANT: Garvin, Michael  
; TITLE OF INVENTION: Compositions and Methods for Increasing Cholesterol Eflux and Raising HDL using ATP Binding Cassette Transporter Protein ABC1  
; TITLE OF INVENTION: Eflux and Raising HDL using ATP Binding Cassette Transporter Protein ABC1  
; FILE REFERENCE: 99\_395-B  
; CURRENT APPLICATION NUMBER: US/09/596,141C  
; CURRENT FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: US 60/140,264  
; PRIOR FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: US 60/153,872  
; PRIOR FILING DATE: 1999-09-14  
; PRIOR APPLICATION NUMBER: US 60/166,573  
; PRIOR FILING DATE: 1999-11-19  
; NUMBER OF SEQ ID NOS: 62  
SEQ ID NO 3  
; LENGTH: 1643  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-56-141C-3

Query Match 48.2%; Score 1394.4%; DB 3; Length 1643;  
Best Local Similarity 97.9%; Pred. 0; Mismatches 6; Indels 26; Gaps 10;

Query Match 48.2%; Score 1394.4%; DB 3; Length 1643;  
Best Local Similarity 97.9%; Pred. 0; Mismatches 6; Indels 26; Gaps 10;

Query Match 48.2%; Score 1394.4%; DB 3; Length 1643;  
Best Local Similarity 97.9%; Pred. 0; Mismatches 6; Indels 26; Gaps 10;

QY 1345 GCCTCCATGCACTTCAGGGCTCTGTCTCTATGCGTCTGCTGTT 1404  
Db 16 GGCTCCATGCACTTCAGGGCTCTGTCTGTTGCCTGTTGTT 73

QY 1405 GATGAACCAACTGATGATGACTGGCTGCGCTGAGATCCRTGACTG 1464  
Db 74 GATGAACCAACTGATGACTGGCTGAGATCCRTGACTG 132

QY 1465 TAGATGGAGGGGCTGTCAGCTGATGCTGCTGCTGTTGGAAT 1524  
Db 133 TAGATGGAGGGCCTCT-CAGCTGATGCTGCTATGAGTGTGTT 191

QY 1525 ATGATGGAGCTGGTGGGGAAAGAAGTAGGTGGGGAGCTCTCATGCCACCTCA 1584  
Db 192 ATGATGGAGCTGGGGAAAGAAGTAGGTGGGGAGCTCTCATGCCACCTCA 251

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 06:52:37 ; Search time 409.228 Seconds  
(without alignments)

14034.494 Million cell updates/sec

Perfect score: US-09-846-456A-1

Sequence: 1 acgggatcggttgcagggt.....gcccacccaccaactt 3231

Scoring table: IDENTITY\_NUC Gapext 1.0

Searched: 1303057 seqs, 88780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing First 45 summaries

Database : Issued Patents NA:\*

```

1: /cgn2_6/picodata/1/in/a/1_COMB.seq:*
2: /cgn2_6/picodata/1/in/a/5_COMB.seq:*
3: /cgn2_6/picodata/1/in/a/6A_COMB.seq:*
4: /cgn2_6/picodata/1/in/H_COMB.seq:*
5: /cgn2_6/picodata/1/in/PCTUS_COMB.seq:*
6: /cgn2_6/picodata/1/in/PP_COMB.seq:*
7: /cgn2_6/picodata/1/in/RE_COMB.seq:*
8: /cgn2_6/picodata/1/in/backfile1.seq:*
9: /cgn2_6/picodata/1/in/backfile1.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1485.4	46.0	1643	3	US-09-596-141C-3	Sequence 1, Appli
2	1485.4	46.0	1643	3	US-09-595-56C-3	Sequence 3, Appli
3	1134.8	35.1	1197	3	US-09-50-312-1	Sequence 1, Appli
4	1347.4	10.8	118143	3	US-09-949-016-17196	Sequence 17196, A
C 5	335.6	10.4	13821	3	US-09-949-016-13990	Sequence 13990, A
C 6	333	10.3	84870	3	US-09-949-016-17547	Sequence 17547, A
7	330.4	10.2	16148	3	US-09-949-016-12969	Sequence 12969, A
8	330	10.2	14519	3	US-09-949-016-15611	Sequence 15611, A
9	330	10.2	14519	3	US-09-949-016-15612	Sequence 15612, A
10	325.2	10.1	31318	3	US-09-949-016-12959	Sequence 12959, A
11	324.8	10.1	31319	3	US-09-949-016-15963	Sequence 15963, A
C 12	324.4	10.0	87734	3	US-09-949-016-17521	Sequence 17521, A
13	323.4	10.0	78530	3	US-09-949-016-16750	Sequence 16750, A
14	323.4	10.0	44019	3	US-09-949-016-14902	Sequence 14902, A
15	321.6	10.0	9208	3	US-09-949-016-15567	Sequence 15567, A
16	319.2	9.9	78631	3	US-09-791-389-3	Sequence 3, Appli
17	319.2	9.9	4441	3	US-09-949-016-15125	Sequence 15125, A
C 18	319	9.9	11543	3	US-09-949-016-12071	Sequence 12071, A
C 19	319	9.9	11543	3	US-09-949-016-12673	Sequence 12673, A
C 20	319	9.9	11544	3	US-09-949-016-16172	Sequence 16172, A
C 21	319	9.9	11544	3	US-09-949-016-16173	Sequence 16173, A
C 22	319	9.9	11544	3	US-09-949-016-16174	Sequence 16174, A
C 23	319	9.9	11544	3	US-09-949-016-16175	Sequence 16175, A
24	318.2	9.8	37292	3	US-09-949-016-15382	Sequence 15382, A

#### ALIGNMENTS

```

RESULT 1
US-09-596-141C-3 Application US/09596141C
; sequence 3, Application US/09596141C
; Patent No. 6821774
; GENERAL INFORMATION:
;   APPLICANT: Lawn, Richard M.
;   APPLICANT: Wade, David
;   APPLICANT: Oran, John F.
;   APPLICANT: Galvin, Michael
; TITLE OF INVENTION: Compositions and Methods for Increasing Cholesterol Eflux and Raising HDL using ATP Binding Cassette Transporter Protein ABC1
; TITLE OF INVENTION: Efflux and Raising HDL using ATP Binding Cassette Transporter Protein ABC1
; FILE REFERENCE: 99-395-B
; CURRENT APPLICATION NUMBER: US/09/596-141C
; CURRENT FILING DATE: 2000-06-16
; PRIORITY NUMBER: US 60/140,264
; PRIORITY NUMBER: US 60/153,872
; PRIORITY NUMBER: US 60/166,573
; PRIORITY NUMBER: US 60/199-11-19
; SEQ ID NO: 62
; SEQ ID NO 3
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-596-141C-3

Query Match 46.0% Score 1485.4; DB 3; Length 1643;
Best Local Similarity 98.1%; Pred. No. 0; Mismatches 6; Indels 26; Gaps 10;
Matches 1615; Conservative 1615; Score 1485.4;
Query Match 46.0% Score 1485.4; DB 3; Length 1643;
Best Local Similarity 98.1%; Pred. No. 0; Mismatches 6; Indels 26; Gaps 10;
Matches 1615; Conservative 1615; Score 1485.4;
Qy 1345 GCCTCCACATGCCCTTCAAGCTGTTCTGGCTTCAGTGTT 1404
Db 16 GGCTCCACATGCCCTTCAAGCTGTTCTGGCTTCAGTGTT 73
Qy 1405 GATAGAACCATGTGATGTGACTCGGGCTTGAGCTGGATCTGTGACTG 1464
Db 74 GATAGAACCATGTGATGTGACTCGGGCTTGAGCTGGATCTGTGACTG 132
Qy 1465 TAGCATGGGGGGCTTCAAGCTGAACTCTGGCTGGGGCTTCAGTGTT 1524
Db 133 TAGCATGGGGGGCTTCAAGCTGAACTCTGGCTGGGGCTTCAGTGTT 191
Qy 1525 ATGATGGAGCTGGAGCTGGAGAGAAGTAGGGCTTGGGGAGCTCTCATGCCACCTCA 1584
Db 192 ATGATGGAGCTGGAGAGAAGTAGGGCTTGGGGAGCTCTCATGCCACCTCA 251
```